

OIPF

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/628,112
DATE: 08/10/2000
TIME: 15:33:16Input Set : A:\JH1120-11.TXT
Output Set : N:\CRF3\08102000\I628112.raw

4 <110> APPLICANT: Lee, Se-Jin
5 McPherron, Alexandra C.
7 <120> TITLE OF INVENTION: PROMYOSTATIN PEPTIDES AND METHODS OF
8 USING SAME
10 <130> FILE REFERENCE: JH1120-11
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/628,112
C--> 12 <141> CURRENT FILING DATE: 2000-07-27
12 <150> PRIOR APPLICATION NUMBER: 09/124,180
13 <151> PRIOR FILING DATE: 1998-07-28
15 <150> PRIOR APPLICATION NUMBER: 09/019,070
16 <151> PRIOR FILING DATE: 1998-02-05
18 <150> PRIOR APPLICATION NUMBER: 08/862,445
19 <151> PRIOR FILING DATE: 1997-05-23
21 <150> PRIOR APPLICATION NUMBER: 08/847,910
22 <151> PRIOR FILING DATE: 1997-04-28
24 <150> PRIOR APPLICATION NUMBER: 08/795,071
25 <151> PRIOR FILING DATE: 1997-02-05
27 <150> PRIOR APPLICATION NUMBER: 08/525,596
28 <151> PRIOR FILING DATE: 1995-10-26
30 <160> NUMBER OF SEQ ID NOS: 29
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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35 <211> LENGTH: 2743
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (59)...(1183)
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45 atg caa aaa ctg caa ctc tgt gtt tat att tac ctg ttt atg ctg att 106
46 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
47 1 5 10 15
49 gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat 154
50 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
51 20 25 30
53 gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act 202
54 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
55 35 40 45
57 aaa tct tca aga ata gaa gcc att aag ata caa atc ctc agt aaa ctt 250
58 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
59 50 55 60
61 cgt ctg gaa aca gct cct aac atc agc aaa gat gtt ata aga caa ctt 298
62 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
63 65 70 75 80
65 tta ccc aaa gct cct cca ctc cgg gaa ctg att gat cag tat gat gtc 346
66 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val

ENTERED

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67	85	90	95	
69	cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac	394		
70	Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His			
71	100 105 110			
73	gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt cta	442		
74	Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu			
75	115 120 125			
77	atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct	490		
78	Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser			
79	130 135 140			
81	aaa ata caa tac aat aaa gta gta aag gcc caa cta tgg ata tat ttg	538		
82	Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu			
83	145 150 155 160			
85	aga ccc gtc gag act cct aca aca gtg ttt gtg caa atc ctg aga ctc	586		
86	Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu			
87	165 170 175			
89	atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg	634		
90	Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu			
91	180 185 190			
93	aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg	682		
94	Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val			
95	195 200 205			
97	aag aca gtg ttg caa aat tgg ctc aaa caa cct gaa tcc aac tta ggc	730		
98	Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly			
99	210 215 220			
101	att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc	778		
102	Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr			
103	225 230 235 240			
105	ttc cca gga cca gga gaa gat ggg ctg aat ccg ttt tta gag gtc aag	826		
106	Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys			
107	245 250 255			
109	gta aca gac aca cca aaa aga tcc aga agg gat ttt ggt ctt gac tgt	874		
110	Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys			
111	260 265 270			
113	gat gag cac tca aca gaa tca cga tgc tgt cgt tac cct cta act gtg	922		
114	Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val			
115	275 280 285			
117	gat ttt gaa gct ttt gga tgg gat tgg att atc gct cct aaa aga tat	970		
118	Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr			
119	290 295 300			
121	aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa	1018		
122	Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			
123	305 310 315 320			
125	tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca	1066		
126	Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala			
127	325 330 335			
129	ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat	1114		
130	Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr			
131	340 345 350			

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133 ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcg atg gta      1162
134 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
135          355          360          365
137 gta gac cgc tgt ggg tgc tca tgagatttat attaagcggt cataacttcc      1213
138 Val Asp Arg Cys Gly Cys Ser
139          370          375
141 taaaacatgg aaggtttttc cctcaacaat tttgaagctg tgaaattaag taccacaggc      1273
142 tataggccta gagtatgcta cagtcaactta agcataagct acagtatgta aactaaaagg      1333
143 gggaaatata gcaatgggtg gcatttaacc atccaaacaa atcatacaag aaagttttat      1393
144 gatttccaga gtttttgagc tagaaggaga tcaaattaca tttatgttcc tatatatattac      1453
145 aacatcggcg aggaaatgaa agcgattctc cttgagttct gatgaattaa aggagtatgc      1513
146 tttaaagtct atttctttta agttttgttt aatattttaca gaaaaatcca catacagtat      1573
147 tggtaaaatg caggattggt atataccatc attcgaatca tccttaaaaca cttgaattta      1633
148 tattgtatgg tagtatactt ggtaagataa aattccacaa aaatagggat ggtgcagcat      1693
149 atgcaatttc cattcctatt ataattgaca cagtacatta acaatccatg ccaacgggtgc      1753
150 taatacgata ggctgaatgt ctgaggctac caggtttatc acataaaaaa cattcagtaa      1813
151 aatagtaagt ttctcttttc ttcaggtgca ttttcttaca cctccaaatg aggaatggat      1873
152 tttctttaat gtaagaagaa tcatttttct agaggtttgc tttcaattct gtagcatact      1933
153 tggagaaact gcattatctt aaaaggcagt caaatgggtg ttgtttttat caaaatgtca      1993
154 aaataacata ctgggagaag tatgtaattt tgtctttgga aaattacaac actgcctttg      2053
155 caacactgca gtttttatgg taaaaataa gaaatgatcg actctatcaa tattgtataa      2113
156 aaagactgaa acaatgcatt tatataatat gtatacaata ttgtttttgta aataagtgtc      2173
157 tcctttttta ttacttttgg tatattttta cactaaggac atttcaaatt aagtactaag      2233
158 gcacaaagac atgtcatgca tcacagaaaa gcaactactt atatttcaga gcaaatttag      2293
159 agattaaata gtggtcttaa aactccatat gttaatgatt agatggttat attacaatca      2353
160 ttttatattt ttttacatga ttaacattca cttatggatt catgatggct gtataaagtg      2413
161 aatttgaaat ttcaatgggt tactgtcatt gtgttttaaa ctcaacgttc cattatttta      2473
162 atacttgcaa aaacattact aagtatacca aaataattga ctctattatc tgaaatgaag      2533
163 aataaactga tgctatctca acaataactg ttacttttat tttataattt gataatgaat      2593
164 atatttctgc atttttttac ttctgttttg taaattggga ttttgttaat caaattttatt      2653
165 gtactatgac taaatgaaat tatttcttac atctaatttg tagaaacagt ataagttata      2713
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168 <210> SEQ ID NO: 2
169 <211> LENGTH: 375
170 <212> TYPE: PRT
171 <213> ORGANISM: Homo sapiens
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176 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
177 20 25 30
178 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
179 35 40 45
180 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
181 50 55 60
182 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
183 65 70 75 80
184 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
185 85 90 95

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186 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
187                               100           105           110
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189                               115           120           125
190 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
191                               130           135           140
192 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
193 145                               150           155           160
194 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
195                               165           170           175
196 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
197                               180           185           190
198 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
199                               195           200           205
200 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
201                               210           215           220
202 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
203 225                               230           235           240
204 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
205                               245           250           255
206 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
207                               260           265           270
208 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
209                               275           280           285
210 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
211                               290           295           300
212 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
213 305                               310           315           320
214 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
215                               325           330           335
216 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
217                               340           345           350
218 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
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224 <211> LENGTH: 2676
225 <212> TYPE: DNA
226 <213> ORGANISM: Mus musculus
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (104)...(1231)
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234 aaataagaac aagggaaaaa aaaagattgt gctgattttt aaa atg atg caa aaa      115
235                               Met Met Gln Lys
236                               1
238 ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc      163

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239	Leu	Gln	Met	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile	Ala	Ala	Gly	
240	5					10				15						20	
242	cca	gtg	gat	cta	aat	gag	ggc	agt	gag	aga	gaa	gaa	aat	gtg	gaa	aaa	211
243	Pro	Val	Asp	Leu	Asn	Glu	Gly	Ser	Glu	Arg	Glu	Glu	Asn	Val	Glu	Lys	
244					25					30						35	
246	gag	ggg	ctg	tgt	aat	gca	tgt	gcg	tgg	aga	caa	aac	acg	agg	tac	tcc	259
247	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn	Thr	Arg	Tyr	Ser	
248				40					45					50			
250	aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agt	aag	ctg	cgc	ctg	gaa	307
251	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu	
252			55				60						65				
254	aca	gct	cct	aac	atc	agc	aaa	gat	gct	ata	aga	caa	ctt	ctg	cca	aga	355
255	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Arg	
256		70				75						80					
258	gcg	cct	cca	ctc	cgg	gaa	ctg	atc	gat	cag	tac	gac	gtc	cag	agg	gat	403
259	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp	
260	85					90				95						100	
262	gac	agc	agt	gat	ggc	tct	ttg	gaa	gat	gac	gat	tat	cac	gct	acc	acg	451
263	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr	
264				105					110					115			
266	gaa	aca	atc	att	acc	atg	cct	aca	gag	tct	gac	ttt	cta	atg	caa	gcg	499
267	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	Met	Gln	Ala	
268				120					125					130			
270	gat	ggc	aag	ccc	aaa	tgt	tgc	ttt	ttt	aaa	ttt	agc	tct	aaa	ata	cag	547
271	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln	
272		135				140						145					
274	tac	aac	aaa	gta	gta	aaa	gcc	caa	ctg	tgg	ata	tat	ctc	aga	ccc	gtc	595
275	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val	
276		150				155						160					
278	aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	atc	aaa	ccc	643
279	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro	
280	165					170				175					180		
282	atg	aaa	gac	ggg	aca	agg	tat	act	gga	atc	cga	tct	ctg	aaa	ctt	gac	691
283	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp	
284				185					190					195			
286	atg	agc	cca	ggc	act	ggg	att	tgg	cag	agt	att	gat	gtg	aag	aca	gtg	739
287	Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val	
288			200						205					210			
290	ttg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aac	tta	ggc	att	gaa	atc	787
291	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile	
292			215				220						225				
294	aaa	gct	ttg	gat	gag	aat	ggc	cat	gat	ctt	gct	gta	acc	ttc	cca	gga	835
295	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly	
296		230				235						240					
298	cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc	aag	gtg	aca	gac	883
299	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	
300	245					250				255					260		
302	aca	ccc	aag	agg	tcc	cgg	aga	gac	ttt	ggg	ctt	gac	tgc	gat	gag	cac	931
303	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
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